**What is claimed is:**

1. A molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP binding pocket, wherein the TMP binding pocket comprises the amino acids listed in Table 1, the TMP binding pocket being defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by the structure coordinates listed in Figure 2.

2. The molecule or molecular complex of claim 1, wherein the TMP binding pocket comprises the amino acids listed in Table 2.

3. The molecule or molecular complex of claim 1, wherein the TMP binding pocket comprises the amino acids listed in Table 3.

4. A molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase TMP/ATP substrate binding pocket, wherein the TMP substrate binding pocket comprises the amino acids listed in Table 4, the substrate binding pocket being defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by the structure coordinates listed in Figure 2.

5. The molecule or molecular complex of claim 4, wherein the TMP/ATP binding pocket comprises the amino acids listed in Table 5.

6. The molecule or molecular complex of claim 4, wherein the TMP/ATP binding pocket comprises the amino acids listed in Table 6.

7. A molecule or molecular complex that is structurally homologous to an *S. aureus* thymidylate kinase molecule or molecular complex, wherein the *S. aureus*

thymidylate kinase molecule or molecular complex is represented by at least a portion of the structure coordinates listed in Figure 2.

8. A scalable three dimensional configuration of points, at least a portion of said points derived from structure coordinates of at least a portion of an *S. aureus* thymidylate kinase molecule or molecular complex listed in Figure 2 comprising at least one of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP or TMP/ATP binding pocket.

9. The scalable three dimensional configuration of points of claim 8, wherein substantially all of said points are derived from structure coordinates of an *S. aureus* thymidylate kinase molecule or molecular complex listed in Figure 2.

10. The scalable three dimensional configuration of points of claim 8 wherein at least a portion of the points derived from the *S. aureus* thymidylate kinase structure coordinates are derived from structure coordinates representing the locations of at least the backbone atoms of amino acids defining an *S. aureus* thymidylate kinase TMP binding pocket, the TMP binding pocket comprising the amino acids listed in Table 1.

11. The scalable three dimensional configuration of points of claim 10, wherein the TMP binding pocket comprises the amino acids listed in Table 2.

12. The scalable three dimensional configuration of points of claim 10, wherein the TMP binding pocket comprises the amino acids listed in Table 3.

13. The scalable three dimensional configuration of points of claim 8 wherein at least a portion of the points derived from the *S. aureus* thymidylate kinase structure coordinates are derived from structure coordinates representing the locations of at least the backbone atoms of amino acids defining an *S. aureus* thymidylate kinase

TMP/ATP binding pocket, the TMP/ATP substrate binding pocket comprising the amino acids listed in Table 4.

14. The scalable three dimensional configuration of points of claim 13, wherein the TMP/ATP binding pocket comprises the amino acids listed in Table 5.

15. The scalable three dimensional configuration of points of claim 13, wherein the TMP/ATP binding pocket comprises the amino acids listed in Table 6.

16. The scalable three dimensional configuration of points of claim 8 displayed as a holographic image, a stereodiagram, a model or a computer-displayed image.

17. A scalable three dimensional configuration of points, at least a portion of the points derived from structure coordinates of at least a portion of a molecule or a molecular complex that is structurally homologous to an *S. aureus* thymidylate kinase molecule or molecular complex and comprises at least one of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP or TMP/ATP binding pocket.

18. The scalable three-dimensional configuration of points of claim 17 displayed as a holographic image, a stereodiagram, a model or a computer-displayed image

19. A machine-readable data storage medium comprising a data storage material encoded with machine readable data which, when using a machine programmed with instructions for using said data, is capable of displaying a graphical three-dimensional representation of at least one molecule or molecular complex selected from the group consisting of:

(i) a molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP binding pocket comprising the amino acids listed in Table 1, the TMP binding pocket defined by a set of points having a root mean square deviation of less than about 2.1 Å from

points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Figure 2;

(ii) a molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP/ATP binding pocket comprising the amino acids listed in Table 4, the TMP/ATP binding pocket defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Figure 2; and

(iii) a molecule or molecular complex that is structurally homologous to an *S. aureus* thymidylate kinase molecule or molecular complex, wherein the *S. aureus* thymidylate kinase molecule or molecular complex is represented by at least a portion of the structure coordinates listed in Figure 2.

20. A machine-readable data storage medium comprising a data storage material encoded with a first set of machine readable data which, when combined with a second set of machine readable data, using a machine programmed with instructions for using said first set of data and said second set of data, can determine at least a portion of the structure coordinates corresponding to the second set of machine readable data, wherein said first set of data comprises a Fourier transform of at least a portion of the structural coordinates for *S. aureus* thymidylate kinase listed in Figure 2; and said second set of data comprises an x-ray diffraction pattern of a molecule or molecular complex of unknown structure.

21. A method for obtaining structural information about a molecule or a molecular complex of unknown structure comprising:

crystallizing the molecule or molecular complex;

generating an x-ray diffraction pattern from the crystallized molecule or molecular complex;

applying at least a portion of the structure coordinates set forth Figure 2 to the x-ray diffraction pattern to generate a three-dimensional electron density map of at least a portion of the molecule or molecular complex whose structure is unknown.

22. A method for homology modeling an *S. aureus* thymidylate kinase homolog comprising:

aligning the amino acid sequence of an *S. aureus* thymidylate kinase homolog with an amino acid sequence of *S. aureus* thymidylate kinase and incorporating the sequence of the *S. aureus* thymidylate kinase homolog into a model of *S. aureus* thymidylate kinase derived from structure coordinates set forth in Figure 2 to yield a preliminary model of the *S. aureus* thymidylate kinase homolog;

subjecting the preliminary model to energy minimization to yield an energy minimized model;

remodeling regions of the energy minimized model where stereochemistry restraints are violated to yield a final model of the *S. aureus* thymidylate kinase homolog.

23. A computer-assisted method for identifying an inhibitor of *S. aureus* thymidylate kinase activity comprising:

supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP binding pocket, the TMP binding pocket comprising the amino acids listed in Table 1;

supplying the computer modeling application with a set of structure coordinates of a chemical entity; and

determining whether the chemical entity is an inhibitor expected to bind to or interfere with the molecule or molecular complex, wherein binding to or

interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* thymidylate kinase activity.

24. A computer-assisted method for identifying an inhibitor of *S. aureus* thymidylate kinase activity comprising:

supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP/ATP binding pocket, the TMP/ATP binding pocket comprising the amino acids listed in Table 4;

supplying the computer modeling application with a set of structure coordinates of a chemical entity; and

determining whether the chemical entity is an inhibitor expected to bind to or interfere with the molecule or molecular complex, wherein binding to or interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* thymidylate kinase activity.

25. The method of claim 23 wherein the TMP binding pocket comprises the amino acids listed in Table 1, the TMP binding pocket being defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Figure 2.

26. The method of claim 24 wherein the TMP/ATP binding pocket comprises the amino acids listed in Table 4, the TMP/ATP binding pocket being defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Figure 2.

27. The method of claim 23 or 24 wherein determining whether the chemical entity is an inhibitor expected to bind to or interfere with the molecule or molecular complex comprises performing a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex, followed by computationally analyzing the results of the fitting operation to quantify the association between the chemical entity and the binding pocket.

28. The method of claim 23 or 24 further comprising screening a library of chemical entities.

29. A computer-assisted method for designing an inhibitor of *S. aureus* thymidylate kinase activity comprising:

supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP binding pocket, the TMP binding pocket comprising the amino acids listed in Table 1;

supplying the computer modeling application with a set of structure coordinates for a chemical entity;

evaluating the potential binding interactions between the chemical entity and substrate binding pocket of the molecule or molecular complex;

structurally modifying the chemical entity to yield a set of structure coordinates for a modified chemical entity; and

determining whether the modified chemical entity is an inhibitor expected to bind to or interfere with the molecule or molecular complex, wherein binding to or interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* thymidylate kinase activity.

30. A computer-assisted method for designing an inhibitor of *S. aureus* thymidylate kinase activity comprising:

supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP/ATP binding pocket, the TMP/ATP binding pocket comprising the amino acids listed in Table 4;

supplying the computer modeling application with a set of structure coordinates for a chemical entity;

evaluating the potential binding interactions between the chemical entity and substrate binding pocket of the molecule or molecular complex;

structurally modifying the chemical entity to yield a set of structure coordinates for a modified chemical entity; and

determining whether the modified chemical entity is an inhibitor expected to bind to or interfere with the molecule or molecular complex, wherein binding to or interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* thymidylate kinase activity.

31. The method of claim 29 wherein the TMP binding pocket comprises the amino acids listed in Table 1, the TMP binding pocket being defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Figure 2.

32. The method of claim 30 wherein the TMP/ATP binding pocket comprises the amino acids listed in Table 1, the TMP/ATP binding pocket being defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Figure 2.

33. The method of claim 29 or 30 wherein determining whether the modified chemical entity is an inhibitor expected to bind to or interfere with the molecule or

molecular complex comprises performing a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex, followed by computationally analyzing the results of the fitting operation to quantify the association between the chemical entity and the binding pocket.

34. The method of claim 29 or 30 wherein the set of structure coordinates for the chemical entity is obtained from a chemical fragment library

35. A computer-assisted method for designing an inhibitor of *S. aureus* thymidylate kinase activity *de novo* comprising:

supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP binding pocket, wherein the TMP substrate binding pocket comprises the amino acids listed in Table 1;

computationally building a chemical entity represented by set of structure coordinates; and

determining whether the chemical entity is an inhibitor expected to bind to or interfere with the molecule or molecular complex, wherein binding to or interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* thymidylate kinase activity.

36. A computer-assisted method for designing an inhibitor of *S. aureus* thymidylate kinase activity *de novo* comprising:

supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of an *S. aureus* thymidylate kinase or thymidylate kinase-like TMP/ATP binding pocket, wherein the TMP/ATP binding pocket comprises the amino acids listed in Table 4;

computationally building a chemical entity represented by set of structure coordinates; and

determining whether the chemical entity is an inhibitor expected to bind to or interfere with the molecule or molecular complex, wherein binding to or interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* thymidylate kinase activity.

37. The method of claim 35 wherein the TMP binding pocket comprises the amino acids listed in Table 1, the TMP binding pocket being defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Figure 2.

38. The method of claim 36 wherein the TMP/ATP binding pocket comprises the amino acids listed in Table 4, the TMP/ATP binding pocket being defined by a set of points having a root mean square deviation of less than about 2.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Figure 2.

39. The method of claim 35 or 36 wherein determining whether the chemical entity is an inhibitor expected to bind to or interfere with the molecule or molecular complex comprises performing a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex, followed by computationally analyzing the results of the fitting operation to quantify the association between the chemical entity and the binding pocket.

40. The method of any of claims 23, 24, 29, 30, 35, or 36 further comprising supplying or synthesizing the potential inhibitor, then assaying the potential inhibitor to determine whether it inhibits *S. aureus* TMK activity.

41. A method for making an inhibitor of *S. aureus* TMK activity, the method comprising chemically or enzymatically synthesizing a chemical entity to yield an inhibitor of *S. aureus* TMK activity, the chemical entity having been identified during a computer-assisted process comprising supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of at least one of a *S. aureus* thymidylate kinase or thymidylate kinase-like TMP or TMP/ATP binding pocket; supplying the computer modeling application with a set of structure coordinates of a chemical entity; and determining whether the chemical entity is expected to bind to or interfere with the molecule or molecular complex at a binding pocket, wherein binding to or interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* TMK activity.

42. A method for making an inhibitor of *S. aureus* TMK activity, the method comprising chemically or enzymatically synthesizing a chemical entity to yield an inhibitor of *S. aureus* TMK activity, the chemical entity having been designed during a computer-assisted process comprising supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of at least one of a *S. aureus* thymidylate kinase or thymidylate kinase-like TMP or TMP/ATP binding pocket; supplying the computer modeling application with a set of structure coordinates for a chemical entity; evaluating the potential binding interactions between the chemical entity and a binding pocket of the molecule or molecular complex; structurally modifying the chemical entity to yield a set of structure coordinates for a modified chemical entity; and determining whether the chemical entity is expected to bind to or interfere with the molecule or molecular complex at the binding pocket, wherein binding to or interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* TMK activity.

43. A method for making an inhibitor of *S. aureus* TMK activity, the method comprising chemically or enzymatically synthesizing a chemical entity to yield an inhibitor of *S. aureus* TMK activity, the chemical entity having been designed during a computer-assisted process comprising supplying a computer modeling application with a set of structure coordinates of a molecule or molecular complex, the molecule or molecular complex comprising at least a portion of at least one of a *S. aureus* thymidylate kinase or thymidylate kinase-like TMP or TMP/ATP binding pocket; computationally building a chemical entity represented by set of structure coordinates; and determining whether the chemical entity is expected to bind to or interfere with the molecule or molecular complex at a binding pocket, wherein binding to or interfering with the molecule or molecular complex is indicative of potential inhibition of *S. aureus* TMK activity.

44. An inhibitor of *S. aureus* thymidylate kinase activity identified, designed or made according to the method of any of the claims 23, 24, 29, 30, 35, 36, 41, 42, or 43.

45. A composition comprising an inhibitor of *S. aureus* thymidylate kinase activity identified or designed according to the method of any of the claims 23, 24, 29, 30, 35, 36, 41, 42, or 43.

46. A pharmaceutical composition comprising an inhibitor of *S. aureus* thymidylate kinase activity identified or designed according to the method of any of the claims 23, 24, 29, 30, 35, 36, 41, 42, or 43 or a salt thereof, and pharmaceutically acceptable carrier.

47. A method for crystallizing an *S. aureus* thymidylate kinase molecule or molecular complex comprising:

preparing purified *S. aureus* thymidylate kinase at a concentration of about 1 mg/ml to about 50 mg/ml; and

crystallizing *S. aureus* thymidylate kinase from a solution comprising about 5 wt. % to about 50 wt. % PEG, about 0.05 M to about 0.5 M $MgCl_2$, and about 0 wt. % to about 20 wt. % DMSO, wherein the solution is buffered to a pH of about 6 to about 7.

48. A method for crystallizing an *S. aureus* thymidylate kinase molecule or molecular complex comprising:

preparing purified *S. aureus* thymidylate kinase at a concentration of about 1 mg/ml to about 50 mg/ml; and

crystallizing *S. aureus* thymidylate kinase from a solution comprising about 2 mM to about 20 mM β,γ-difluoromethylene-bisphosphonate adenosine monophosphate and about 0 wt. % to about 20 wt. % DMSO, wherein the solution is buffered to a pH of about 6 to about 7.

49. A crystal of *S. aureus* thymidylate kinase.

50. The crystal of claim 49 having the trigonal space group symmetry $P2_1$.

51. The crystal of claim 49 comprising a unit cell having dimensions of a, b, and c; wherein a is about 40 Å to about 60 Å, b is about 80 Å to about 100 Å, and c is about 40 Å to about 60 Å; and wherein $\alpha = \gamma = 90^o$ and β is about 80° to about 120°.

52. The crystal of claim 49 comprising atoms arranged in a spatial relationship represented by the structure coordinates listed in Figure 2.

53. The crystal of claim 49 having amino acid sequence SEQ ID NO:1.

54. The crystal of claim 49 having amino acid sequence SEQ ID NO:1, with the proviso that at least one methionine is replaced with selenomethionine.